Amendments to the Specification:

Please replace the paragraph beginning at page 9, line 3, with the following amended paragraph:

--Figure 1: The hairpin ribozyme.

The hairpin ribozyme consists of a 50 to 54 nucleotide RNA molecule (SEQ ID NO:8; shaded, in uppercase letters) which binds and cleaves an RNA substrate (SEQ ID NO:13; lowercase letters). The catalytic RNA folds into a 2-dimensional structure that resembles a hairpin, consisting of two helical domains (Helix 3 and 4) and 3 loops (Loop 2, 3 and 4). Two additional helixes, Helix 1 and 2, form between the ribozyme and its substrate. Recognition of the substrate by the ribozyme is via Watson-Crick base pairing (where N or n = any nucleotide, b = C, G or U and B = the nucleotide complementary to b). The length of Helix 2 is fixed at 4 basepairs and the length of Helix 1 typically varies from 6 to 10 basepairs. The substrate must contain a GUC in Loop 5 for maximal activity, and cleavage occurs immediately 5' of the G as indicated by an arrow. The catalytic, but not substrate binding, activity of the ribozyme can be disabled by mutating the AAA in Loop 2 to CGU.--

Please replace the paragraph beginning at page 11, line 18, with the following amended paragraph:

--~~**Figure 10: Schematic of trans cleavage and ligation**~~ **Figure 10: Schematic of trans cleavage and ligation** (SEQ ID NOS:9-12)

Auto-catalytic ribozyme library is transcribed in vitro and allowed to self-cleave. Self-cleaved, helix 2-charged ribozymes are purified and incubated with the target RNA. Following cleavage of target, a portion of the charged ribozymes will ligate themselves to the cleavage products. These product-ribozyme species are then amplified by reverse transcription and PCR to yield the target specific ribozymes.--

Please replace the paragraph beginning at page 15, line 1, with the following amended paragraph:

--A ribozyme "recognition sequence" or "helix 1" ribozyme domain is the portion of a nucleic acid encoding the ribozyme which is complementary to a target RNA 3' of the cleavage site on the target RNA, *i.e.*, the ribozyme nucleic acid sequences 5' of the ribozyme nucleic acid sub-sequence which aligns with the target cleavage site. A GUC ribozyme typically cleaves an RNA having the sequence ~~NNNBCN*GUCNNNNNNNN (SEQ ID NO:1)~~ NNNBN*GUCNNNNNNNN (SEQ ID NO:14) (where N*G is the cleavage site, B is any of G, U or C, and where N is any of G, U, C, or A). GUA ribozymes typically cleave an RNA target sequence consisting of NNNNN*GUANNNNNNNN~~. (SEQ ID NO:2)~~ (where N*G is the cleavage site and where N is any of G, U, C, or A). A "GUA site" is an RNA sub-sequence which includes the nucleic acids GUA which is cleaved b a GUA ribozyme. A "GUC site" is an RNA sub-sequence which includes the nucleic acids GUC which is cleaved by a GUC ribozyme.--

Please replace the paragraph beginning at page 67, line 18, with the following amended paragraph:

--A "mega primer" is generated in a first round of PCR which comprises an AAV 3'-ITR, a $tRNA^{val}$ promoter and ribozyme library genes, using the primers set 1 and ~~1~~ 2 listed below:

1) 3'- AAV-ITR primer (44 nt)

5' A,GGA,AGA,TCT

CTG,GCG,CGC,TCG,CTC,GCT,CAC,TGA,GGC,CGC,CCG,G (SEQ ID NO:5)

Bgl II site is underlined.

2) 5'-oligo with sequences for $tRNA^{val}$ promoter and ribozyme library genes (tRNA-ribozyme lib PCR, 81 nt)

5'-TAC,CAG,GTA,ATA,TAC,CAC,AAC,GTG,TGT,TTC,TCT,GGT,NNN,BTT, CTN,NNN,NNN,TGG,ATC,CTG,TTT,CCG,CCC,GGT,TTC,GAA,CCG-3' (SEQ ID NO:6).--

Please replace the paragraph beginning at page 68, line 1, with the following amended paragraph:

--1) 3'megaprimer (The product from 1st round PCR)

2) ~~5'-AAVITR~~ 5'-AAV-ITR

5'-AGGAAGATCTCAGCAGCTGCGCGCTCGCTCGCTCACTGAGG-3' (SEQ ID NO:7), Bgl II site is underlined.--

Please replace the paragraph beginning at page 81, line 34, with the following:

--5' Primer (37 nt):

5'GGGTAATACGACTCACTATAG*GGATCC*TCGATGAAGC3' (SEQ ID NO:1)

3' Synth Primer (76 nt):

5'TCGACGCGTACCAGGTAATATACCACAACGTGTGTTTCTCTGGTNNNNTTCTNNNN NNNGCTTCATCGAGGATCCC3' (SEQ ID NO:2)

3' Primer:

5'TCG*ACGCGT***ACCAGGTAATATACCACAACGTGTGTTTCTCTGGT**3' (SEQ ID NO:3)

3' Disabled Primer:

5'TCG*ACGCGT***ACCAGGTAATATACCACAACGTGTGACGCTCTGGT**3' (SEQ ID NO:4)

3'- AAV-ITR primer:

5'AGGA*AGATCT*CTGGCGCGCTCGCTCGCTCACTGAGGCCGCCCGG3' (SEQ ID NO:5)

tRNA-Rz lib primer:

5'TACCAGGTAATATACCACAACGTGTGTTTCTCTGGTNNNBTTCTNNN NNNNTGGATCCTGTTTCCGCCCGGTTTCGAACCG3' (SEQ ID NO:6)

5'-AAV-ITR primer:

5'-AGGA*AGATCT*CAGCAGCTGCGCGCTCGCTCGCTCACTGAGG-3' (SEQ ID NO:7)--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 4, at the end of the application.